

SYR-HDAC-5003-U.ST25
SEQUENCE LISTING

<110> SYRRX, INC.
 <120> HISTONE DEACETYLASE INHIBITORS
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 <140> Not Yet Assigned
 <141> 2003-10-09
 <150> 60/419,929
 <151> 2002-10-21
 <160> 3
 <170> PatentIn version 3.1
 <210> 1
 <211> 377
 <212> PRT
 <213> Homo sapiens
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 <221> Amino acid sequence for full length human wild type HDAC8
 <222> (1)..(377)
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 <308> Genbank Accession Number NP_060956
 <309> 2001-02-26
 <313> (1)..(377)
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 1 5 10 15
 Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala
 20 25 30
 Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr
 35 40 45
 Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met
 50 55 60
 Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln
 65 70 75 80
 Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr
 85 90 95
 Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala
 100 105 110

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Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp
115 120 125

Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala
130 135 140

Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu
145 150 155 160

Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp
165 170 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr
180 185 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe
195 200 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Trp Tyr
210 215 220

Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr
225 230 235 240

Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn
245 250 255

Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp
260 265 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu
275 280 285

Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly
290 295 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly
305 310 315 320

Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe
325 330 335

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys
340 345 350

Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr
355 360 365

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Ile Lys Gly Asn Leu Lys His Val Val
370 375

<210> 2
<211> 1134
<212> DNA
<213> Homo sapiens

<220>
<221> Human cDNA sequence encoding residues 1-377 of HDAC8
<222> (1)..(1134)
<223>

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<308> Genbank Accession Number NM_018486
<309> 2001-02-26
<313> (1)..(1134)

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gtgcattctt tgattgaagc atatgcactg cataagcaga tgaggatagt taagcctaaa 180
gtggcctcca tggaggagat ggccaccttc cacactgatg cttatctgca gcatctccag 240
aaggtcagcc aagagggcga tgatgatcat ccggactcca tagaatatgg gctaggttat 300
gactgcccag ccactgaagg gatatttgac tatgcagcag ctataggagg ggctacgatac 360
acagctgccc aatgcctgat tgacggaatg tgcaaagtag caattaactg gtctggaggg 420
tggcatcatg caaagaaaga tgaagcatct gggtttttgtt atctcaatga tgctgtcctg 480
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catggagatg gtgtagaaga cgcattcagt ttcacctcca aagtcatgac cgtgtccctg 600
cacaaattct ccccaggatt tttcccagga acaggtgacg tgtctgatgt tggcctaggg 660
aagggatggg actacagtgt aaatgtgccc attcaggatg gcatacaaga tgaaaaatat 720
taccagatct gtgaaagcgt actaaaggaa gtataccaag cctttaatcc caaagcagtg 780
gtcttacagc tgggagctga cacaatagct ggggatccca tgtgtctcctt taacatgact 840
ccagtgggaa ttggcaagtg tcttaagtac atccttcaat ggcagttggc aacactcatt 900
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cgaatccaac aaatcctcaa ctacatcaaa gggaatctga agcatgtggt ctatg 1134

<210> 3
<211> 385
<212> PRT

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<213> Homo sapiens

<220>

<221> Amino acid sequence for residues 1-377 of HDAC8 with a cleavable N-terminal 6x-histidine tag

<222> (1)..(385)

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<221> Cleavable N-terminal 6x-histidine tag

<222> (1)..(8)

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Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp
85 90 95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
180 185 190

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Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
325 330 335

Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
370 375 380

Val
385